



SEQUENCE LISTING

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MORIMOTO, IKUO  
MIYAMURA, KOICHI

<120> CELL SEPARATION DEVICE AND SEPARATION METHOD

<130> ASAHI-1-PC-1

<140> 09/701,001

<141> 2000-11-22

<150> PCT/JP99/02711

<151> 1999-05-24

<150> JP 159957

<151> 1998-05-25

<150> JP 163023

<151> 1998-05-26

<160> 66

<170> PatentIn Ver. 2.1

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<212> PRT

<213> Mus sp.

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Asp Tyr Val Ile Asn  
1 5

*see EP 0365,205  
Figs 2 and 3  
= CDR1 of anti Lew 3a*

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Glu Ile Tyr Pro Gly Ser Gly Ser Ala Tyr Tyr Asn Glu Met Phe Lys  
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Gly

*= CDR2 of anti Lew 3a*

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Arg Gly Thr Gly Thr Gly Phe Ala Tyr  
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*= CDR3 of anti Lew 3a*

*H chain  
CDR1*

*H chain  
CDR2*

*H chain  
CDR3*

*L chain*  
*CDR 1*  
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 Lys Ala Ser Gln Ser Val Asp Tyr Asp Gly Asp Ser Tyr Met Asn  
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*CDR 1 of anti-Law-Ba*

*L chain*  
*CDR 2*  
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 Ala Ala Ser Asn Leu Glu Ser  
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*CDR 2 of anti-Law-Ba*

*L chain*  
*CDR 3*  
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 Pro Glu Leu Val Lys Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala  
 1 5 10 15  
 tct gga tac aca ttc act gac tat gtt ata aac tgg ttg aac cag aga 96  
 Ser Gly Tyr Thr Phe Thr Asp Tyr Val Ile Asn Trp Leu Asn Gln Arg  
 20 25 30  
 act gga cag ggc ctt gag tgg att gga gag att tat cct gga agt ggt 144  
 Thr Gly Gln Gly Leu Glu Trp Ile Gly Glu Ile Tyr Pro Gly Ser Gly  
 35 40 45  
 agt gct tac tac aat gag atg ttc aag ggc aag gcc aca ctg act gca 192  
 Ser Ala Tyr Tyr Asn Glu Met Phe Lys Gly Lys Ala Thr Leu Thr Ala  
 50 55 60

gac aaa tcc tcc aac aca gcc tac atg cag ctc agc agc ctg aca tct 240  
 Asp Lys Ser Ser Asn Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser  
 65 70 75 80

gag gac tct gcg gtc tat ttc tgt gca aga cgc gga act ggg acg ggg 288  
 Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg Arg Gly Thr Gly Thr Gly  
 85 90 95

ttt gct tac tgg ggc cga ggg act ctg gtc act gtc tct gca 330  
 Phe Ala Tyr Trp Gly Arg Gly Thr Leu Val Thr Val Ser Ala  
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<222> (1) .. (309)

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gcc agc caa agt gtt gat tat gat ggt gat agt tat atg aac tgg tac 96  
 Ala Ser Gln Ser Val Asp Tyr Asp Gly Asp Ser Tyr Met Asn Trp Tyr  
 20 25 30

caa cag aaa cca gga cag cca ccc aaa ctc ctc atc tat gct gca tcc 144  
 Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Ala Ala Ser  
 35 40 45

aat cta gaa tct ggg atc cca gcc agg ttt agt ggc agt ggg tct ggg 192  
 Asn Leu Glu Ser Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly  
 50 55 60

aca gac ttc acc ctc aac atc cat cct gtg gag gag gag gat gct gca 240  
 Thr Asp Phe Thr Leu Asn Ile His Pro Val Glu Glu Glu Asp Ala Ala  
 65 70 75 80

acc tat tac tgt cag caa agt agt gag gat cct ccg acg ttc ggt gga 288  
 Thr Tyr Tyr Cys Gln Gln Ser Ser Glu Asp Pro Pro Thr Phe Gly Gly  
 85 90 95

ggc acc aag ctg gaa atc aaa 309  
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*single chain Ab to CD4*

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Met	Lys	Tyr	Leu	Leu	Pro	Thr	Ala	Ala	Ala	Gly	Leu	Leu	Leu	Leu	Ala	
1				5					10					15		
gcc	cag	ccg	gcc	atg	gcc	gac	att	gtg	ctg	acc	caa	tct	cca	gct	tct	96
Ala	Gln	Pro	Ala	Met	Ala	Asp	Ile	Val	Leu	Thr	Gln	Ser	Pro	Ala	Ser	
		20						25					30			
ttg	gct	gtg	tct	cta	ggg	cag	agg	gcc	acc	atc	tcc	tgc	aag	gcc	agc	144
Leu	Ala	Val	Ser	Leu	Gly	Gln	Arg	Ala	Thr	Ile	Ser	Cys	Lys	Ala	Ser	
		35					40					45				
caa	agt	gtt	gat	tat	gat	ggt	gat	agt	tat	atg	aac	tgg	tac	caa	cag	192
Gln	Ser	Val	Asp	Tyr	Asp	Gly	Asp	Ser	Tyr	Met	Asn	Trp	Tyr	Gln	Gln	
	50					55					60					
aaa	cca	gga	cag	cca	ccc	aaa	ctc	ctc	atc	tat	gct	gca	tcc	aat	cta	240
Lys	Pro	Gly	Gln	Pro	Pro	Lys	Leu	Leu	Ile	Tyr	Ala	Ala	Ser	Asn	Leu	
65					70				75					80		
gaa	tct	ggg	atc	cca	gcc	agg	ttt	agt	ggc	agt	ggg	tct	ggg	aca	gac	288
Glu	Ser	Gly	Ile	Pro	Ala	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	
				85				90						95		
ttc	acc	ctc	aac	atc	cat	cct	gtg	gag	gag	gag	gat	gct	gca	acc	tat	336
Phe	Thr	Leu	Asn	Ile	His	Pro	Val	Glu	Glu	Glu	Asp	Ala	Ala	Thr	Tyr	
		100					105						110			
tac	tgt	cag	caa	agt	agt	gag	gat	cct	ccg	acg	ttc	ggt	gga	ggc	acc	384
Tyr	Cys	Gln	Gln	Ser	Ser	Glu	Asp	Pro	Pro	Thr	Phe	Gly	Gly	Gly	Thr	
		115				120						125				
aag	ctg	gaa	atc	aaa	ggt	gga	ggc	ggt	tca	ggc	gga	ggt	ggc	tcc	gga	432
Lys	Leu	Glu	Ile	Lys	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	
130					135			140								
ggt	ggc	gga	tgc	cag	gtt	cag	ctg	cag	cag	tct	gga	cct	gag	ctg	gtg	480
Gly	Gly	Gly	Ser	Gln	Val	Gln	Leu	Gln	Gln	Ser	Gly	Pro	Glu	Leu	Val	
145				150				155						160		
aag	cct	ggg	gct	tca	gtg	aag	atg	tcc	tgc	aag	gct	tct	gga	tac	aca	528
Lys	Pro	Gly	Ala	Ser	Val	Lys	Met	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	
				165				170						175		
ttc	act	gac	tat	gtt	ata	aac	tgg	ttg	aac	cag	aga	act	gga	cag	ggc	576
Phe	Thr	Asp	Tyr	Val	Ile	Asn	Trp	Leu	Asn	Gln	Arg	Thr	Gly	Gln	Gly	
		180				185						190				
ctt	gag	tgg	att	gga	gag	att	tat	cct	gga	agt	ggt	agt	gct	tac	tac	624
Leu	Glu	Trp	Ile	Gly	Glu	Ile	Tyr	Pro	Gly	Ser	Gly	Ser	Ala	Tyr	Tyr	
	195				200			205								

*CD R 2*

aat gag atg ttc aag ggc aag gcc aca ctg act gca gac aaa tcc tcc 672  
 Asn Glu Met Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser  
 210 215 220

aac aca gcc tac atg cag ctc agc agc ctg aca tct gag gac tct gcg 720  
 Asn Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala  
 225 230 235 240

gtc tat ttc tgt gca aga cgc gga act ggg acg ggg ttt gct tac tgg 768  
 Val Tyr Phe Cys Ala Arg Arg Gly Thr Gly Thr Gly Phe Ala Tyr Trp  
 245 250 255

ggc cga ggg act ctg gtc act gtc tct gca gcg gcc gca gac tac aag 816  
 Gly Arg Gly Thr Leu Val Thr Val Ser Ala Ala Ala Asp Tyr Lys  
 260 265 270

gat gac gat gac aaa ggc tcg agc gag cag aag ctg atc agc gaa gag 864  
 Asp Asp Asp Asp Lys Gly Ser Ser Glu Gln Lys Leu Ile Ser Glu Glu  
 275 280 285

gat ctg ggc tcg agg tcg acc cac cat cat cat cac cac ggg tcg acc 912  
 Asp Leu Gly Ser Arg Ser Thr His His His His His His Gly Ser Thr  
 290 295 300

aaa tgataagctt 925  
 Lys  
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 1 5 10 15

gcc cag ccg gcc atg gcc cag gtt cag ctg cag cag tct gga cct gag 96  
 Ala Gln Pro Ala Met Ala Gln Val Gln Leu Gln Gln Ser Gly Pro Glu  
 20 25 30

ctg gtg aag cct ggg gct tca gtg aag atg tcc tgc aag gct tct gga 144  
 Leu Val Lys Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly  
 35 40 45

tac aca ttc act gac tat gtt ata aac tgg ttg aac cag aga act gga 192  
 Tyr Thr Phe Thr Asp Tyr Val Ile Asn Trp Leu Asn Gln Arg Thr Gly  
 50 55 60

cag ggc ctt gag tgg att gga gag att tat cct gga agt ggt agt gct 240  
 Gln Gly Leu Glu Trp Ile Gly Glu Ile Tyr Pro Gly Ser Gly Ser Ala  
 65 70 75 80

tac	tac	aat	gag	atg	ttc	aag	ggc	aag	gcc	aca	ctg	act	gca	gac	aaa	288
Tyr	Tyr	Asn	Glu	Met	Phe	Lys	Gly	Lys	Ala	Thr	Leu	Thr	Ala	Asp	Lys	
				85					90						95	
tcc	tcc	aac	aca	gcc	tac	atg	cag	ctc	agc	agc	ctg	aca	tct	gag	gac	336
Ser	Ser	Asn	Thr	Ala	Tyr	Met	Gln	Leu	Ser	Ser	Leu	Thr	Ser	Glu	Asp	
			100					105					110			
tct	gcg	gtc	tat	ttc	tgt	gca	aga	cgc	gga	act	ggg	acg	ggg	ttt	gct	384
Ser	Ala	Val	Tyr	Phe	Cys	Ala	Arg	Arg	Gly	Thr	Gly	Thr	Gly	Phe	Ala	
		115					120					125				
tac	tgg	ggc	cga	ggg	act	ctg	gtc	act	gtc	tct	gca	ggg	gga	ggc	ggg	432
Tyr	Trp	Gly	Arg	Gly	Thr	Leu	Val	Thr	Val	Ser	Ala	Gly	Gly	Gly	Gly	
	130					135					140					
tca	ggc	gga	ggt	ggc	tcc	gga	ggt	ggc	gga	tcg	gac	att	gtg	ctg	acc	480
Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Asp	Ile	Val	Leu	Thr	
	145				150					155					160	
caa	tct	cca	gct	tct	ttg	gct	gtg	tct	cta	ggg	cag	agg	gcc	acc	atc	528
Gln	Ser	Pro	Ala	Ser	Leu	Ala	Val	Ser	Leu	Gly	Gln	Arg	Ala	Thr	Ile	
				165					170					175		
tcc	tgc	aag	gcc	agc	caa	agt	gtt	gat	tat	gat	ggg	gat	agt	tat	atg	576
Ser	Cys	Lys	Ala	Ser	Gln	Ser	Val	Asp	Tyr	Asp	Gly	Asp	Ser	Tyr	Met	
			180					185					190			
aac	tgg	tac	caa	cag	aaa	cca	gga	cag	cca	ccc	aaa	ctc	ctc	atc	tat	624
Asn	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Pro	Pro	Lys	Leu	Leu	Ile	Tyr	
		195					200					205				
gct	gca	tcc	aat	cta	gaa	tct	ggg	atc	cca	gcc	agg	ttt	agt	ggc	agt	672
Ala	Ala	Ser	Asn	Leu	Glu	Ser	Gly	Ile	Pro	Ala	Arg	Phe	Ser	Gly	Ser	
	210					215					220					
ggg	tct	ggg	aca	gac	ttc	acc	ctc	aac	atc	cat	cct	gtg	gag	gag	gag	720
Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Asn	Ile	His	Pro	Val	Glu	Glu	Glu	
	225				230				235						240	
gat	gct	gca	acc	tat	tac	tgt	cag	caa	agt	agt	gag	gat	cct	ccg	acg	768
Asp	Ala	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Ser	Ser	Glu	Asp	Pro	Pro	Thr	
				245					250					255		
ttc	ggg	gga	ggc	acc	aag	ctg	gaa	atc	aaa	gcg	gcc	gca	gac	tac	aag	816
Phe	Gly	Gly	Gly	Thr	Lys	Leu	Glu	Ile	Lys	Ala	Ala	Ala	Asp	Tyr	Lys	
			260					265					270			
gat	gac	gat	gac	aaa	ggc	tcg	agc	gag	cag	aag	ctg	atc	agc	gaa	gag	864
Asp	Asp	Asp	Asp	Lys	Gly	Ser	Ser	Glu	Gln	Lys	Leu	Ile	Ser	Glu	Glu	
			275				280					285				
gat	ctg	ggc	tcg	agg	tcg	acc	cac	cat	cat	cat	cac	cac	ggg	tcg	acc	912
Asp	Leu	Gly	Ser	Arg	Ser	Thr	His	His	His	His	His	His	Gly	Ser	Thr	
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aaa tgataagctt  
Lys  
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<212> DNA  
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DNA primer for PCR

<400> 11  
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 DNA primer for PCR

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<210> 19  
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<220>  
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 DNA primer for PCR

<400> 19  
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<210> 20  
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 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Single strand  
 DNA primer for PCR

<400> 20  
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<210> 21  
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 <212> DNA  
 <213> Artificial Sequence

<220>  
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 DNA primer for PCR

<400> 21  
 tcatgaaata cctgctgccg accgctgctg ctggctctgct gctcctcgcg gccag 56

<210> 22  
 <211> 56  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Single strand  
         DNA primer for PCR

<400> 22  
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<210> 23  
 <211> 56  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Single strand  
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<400> 23  
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<210> 24  
 <211> 57  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Single strand  
         DNA primer for PCR

<400> 24  
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<210> 25  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Single strand  
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<400> 25  
 tgcggccgca gactacaagg atg 23

<210> 26  
 <211> 56  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Single strand  
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<400> 26  
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<210> 27  
 <211> 38  
 <212> DNA  
 <213> Artificial Sequence

<220>  
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 DNA primer for PCR

<400> 27  
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<210> 28  
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<220>  
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 DNA primer for PCR

<400> 28  
 ctccggagcc acctccgct gaaccgcctc cacctttgat ttccagcttg gtgcctcc 58

<210> 29  
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 <212> DNA  
 <213> Artificial Sequence

<220>  
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 DNA primer for PCR

<400> 29  
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<210> 30  
 <211> 31  
 <212> DNA  
 <213> Artificial Sequence

<220>  
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 DNA primer for PCR

<400> 30  
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<210> 31  
 <211> 35  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Single strand  
DNA primer for PCR

<400> 31

agccggccat ggcccagggtt cagctgcagc agtct

35

<210> 32

<211> 56

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Single strand  
DNA primer for PCR

<400> 32

ctccggagcc acctccgcct gaaccgcctc cacctgcaga gacagtgacc agagtc

56

<210> 33

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Single strand  
DNA primer for PCR

<400> 33

ctccggaggt ggcggatcgg acattgtgct gacccaatct cca

43

<210> 34

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Single strand  
DNA primer for PCR

<400> 34

tgcggccgct ttgatttcca gcttggtgcc tcc

33

<210> 35

<211> 118

<212> PRT

<213> Mus sp.

<400> 35

Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala

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Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr  
20 25 30

Val Ile Asn Trp Leu Asn Gln Arg Thr Gly Gln Gly Leu Glu Trp Ile  
35 40 45

Gly Glu Ile Tyr Pro Gly Ser Gly Ser Ala Tyr Tyr Asn Glu Met Phe  
50 55 60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Asn Thr Ala Tyr  
65 70 75 80

Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys  
85 90 95

Ala Arg Arg Gly Thr Gly Thr Gly Phe Ala Tyr Trp Gly Arg Gly Thr  
100 105 110

Leu Val Thr Val Ser Ala  
115

<210> 36

<211> 111

<212> PRT

<213> Mus sp.

<400> 36

Asp Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly  
1 5 10 15

Gln Arg Ala Thr Ile Ser Cys Lys Ala Ser Gln Ser Val Asp Tyr Asp  
20 25 30

Gly Asp Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro  
35 40 45

Lys Leu Leu Ile Tyr Ala Ala Ser Asn Leu Glu Ser Gly Ile Pro Ala  
50 55 60

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His  
65 70 75 80

Pro Val Glu Glu Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Ser Ser  
85 90 95

Glu Asp Pro Pro Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys  
100 105 110

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<211> 354

<212> DNA

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<220>

<221> CDS

<222> (1)..(354)

<400> 37  
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 Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala  
 1 5 10 15

tca gtg aag atg tcc tgc aag gct tct gga tac aca ttc act gac tat 96  
 Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr  
 20 25 30

gtt ata aac tgg ttg aac cag aga act gga cag ggc ctt gag tgg att 144  
 Val Ile Asn Trp Leu Asn Gln Arg Thr Gly Gln Gly Leu Glu Trp Ile  
 35 40 45

gga gag att tat cct gga agt ggt agt gct tac tac aat gag atg ttc 192  
 Gly Glu Ile Tyr Pro Gly Ser Gly Ser Ala Tyr Tyr Asn Glu Met Phe  
 50 55 60

aag ggc aag gcc aca ctg act gca gac aaa tcc tcc aac aca gcc tac 240  
 Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Asn Thr Ala Tyr  
 65 70 75 80

atg cag ctc agc agc ctg aca tct gag gac tct gcg gtc tat ttc tgt 288  
 Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys  
 85 90 95

gca aga cgc gga act ggg acg ggg ttt gct tac tgg ggc cga ggg act 336  
 Ala Arg Arg Gly Thr Gly Thr Gly Phe Ala Tyr Trp Gly Arg Gly Thr  
 100 105 110

ctg gtc act gtc tct gca 354  
 Leu Val Thr Val Ser Ala  
 115

<210> 38  
 <211> 333  
 <212> DNA  
 <213> Mus sp.

<220>  
 <221> CDS  
 <222> (1)..(333)

<400> 38  
 gac att gtg ctg acc caa tct cca gct tct ttg gct gtg tct cta ggg 48  
 Asp Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly  
 1 5 10 15

cag agg gcc acc atc tcc tgc aag gcc agc caa agt gtt gat tat gat 96  
 Gln Arg Ala Thr Ile Ser Cys Lys Ala Ser Gln Ser Val Asp Tyr Asp  
 20 25 30

ggt gat agt tat atg aac tgg tac caa cag aaa cca gga cag cca ccc 144  
 Gly Asp Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro  
 35 40 45

aaa	ctc	ctc	atc	tat	gct	gca	tcc	aat	cta	gaa	tct	ggg	atc	cca	gcc	192
Lys	Leu	Leu	Ile	Tyr	Ala	Ala	Ser	Asn	Leu	Glu	Ser	Gly	Ile	Pro	Ala	
	50					55					60					
agg	ttt	agt	ggc	agt	ggg	tct	ggg	aca	gac	ttc	acc	ctc	aac	atc	cat	240
Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Asn	Ile	His	
	65				70					75					80	
cct	gtg	gag	gag	gag	gat	gct	gca	acc	tat	tac	tgt	cag	caa	agt	agt	288
Pro	Val	Glu	Glu	Glu	Asp	Ala	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Ser	Ser	
				85					90					95		
gag	gat	cct	ccg	acg	ttc	ggg	gga	ggc	acc	aag	ctg	gaa	atc	aaa		333
Glu	Asp	Pro	Pro	Thr	Phe	Gly	Gly	Gly	Thr	Lys	Leu	Glu	Ile	Lys		
			100					105					110			
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cag	gtg	cag	ctg	aag	cag	tca	gga	cct	ggc	cta	gtg	cag	ccc	tca	cag	48
Cag	Val	Gln	Leu	Lys	Gln	Ser	Gly	Pro	Gly	Leu	Val	Gln	Pro	Ser	Gln	
	1			5				10					15			
agc	ctg	tcc	ttc	atc	tgc	aca	gtc	tct	ggg	ttc	tca	tta	act	agt	cat	96
Ser	Leu	Ser	Phe	Ile	Cys	Thr	Val	Ser	Gly	Phe	Ser	Leu	Thr	Ser	His	
			20					25					30			
ggg	gta	cac	tgg	gtt	cgc	cag	tct	cca	gga	aag	ggg	ctg	gag	tgg	ctg	144
Gly	Val	His	Trp	Val	Arg	Gln	Ser	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Leu	
		35				40						45				
gga	gtg	ata	tgg	ggg	gct	gga	agg	aca	gac	tat	aat	gca	gct	ttc	ata	192
Gly	Val	Ile	Trp	Gly	Ala	Gly	Arg	Thr	Asp	Tyr	Asn	Ala	Ala	Phe	Ile	
	50				55						60					
tcc	aga	ctg	agc	atc	agc	agg	gac	att	tcc	aag	agc	caa	gtt	ttc	ttt	240
Ser	Arg	Leu	Ser	Ile	Ser	Arg	Asp	Ile	Ser	Lys	Ser	Gln	Val	Phe	Phe	
	65				70					75					80	
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 Asp Val Val Met Thr Gln Thr Pro Leu Ser Leu Pro Val Ser Leu Gly  
 1 5 10 15

gat cag gcc tcc atc tct tgc aga tct agt cag aac ctt gta cac agt 96  
 Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Asn Leu Val His Ser  
 20 25 30

aat gga aat acc tat tta cat tgg tac ctg cag aag cca ggc cag tct 144  
 Asn Gly Asn Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro Gly Gln Ser  
 35 40 45

cca aat ctc ctg atc tac aaa gtt tcc aac cga ttt tct ggg gtc cca 192  
 Pro Asn Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro  
 50 55 60

gac agg ttc agt ggc agt gga tca ggg aca gaa ttc aca ctc aag atc 240  
 Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Lys Ile  
 65 70 75 80

agc aga gtg gag gct gag gat ctg gga gtt tat ttc tgc tct caa agt 288  
 Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Phe Cys Ser Gln Ser  
 85 90 95

aca cat gtt ccg ctc acg ttc ggt gct ggg acc aag gtg gag ctg aaa 336  
 Thr His Val Pro Leu Thr Phe Gly Ala Gly Thr Lys Val Glu Leu Lys  
 100 105 110

cgg 339  
 Arg

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 Met Thr Met Ile Thr Pro Ser Phe Gly Ala Phe Phe Leu Glu Ile Phe  
 1 5 10 15



aac	gtg	aaa	aaa	tta	tta	ttc	gca	att	cct	tta	gtt	gtt	cct	ttc	tat	96
Asn	Val	Lys	Lys	Leu	Leu	Phe	Ala	Ile	Pro	Leu	Val	Val	Pro	Phe	Tyr	
			20					25					30			
gcg	gcc	cag	ccg	gcc	atg	gcc	cag	gtg	aag	ctg	cag	cag	tct	gga	cct	144
Ala	Ala	Gln	Pro	Ala	Met	Ala	Gln	Val	Lys	Leu	Gln	Gln	Ser	Gly	Pro	
		35					40					45				
ggc	cta	gtg	cag	ccc	tca	cag	agc	ctg	tcc	ttc	atc	tgc	aca	gtc	tct	192
Gly	Leu	Val	Gln	Pro	Ser	Gln	Ser	Leu	Ser	Phe	Ile	Cys	Thr	Val	Ser	
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ggg	ttc	tca	tta	act	agt	cat	ggg	gta	cac	tgg	gtt	cgc	cag	tct	cca	240
Gly	Phe	Ser	Leu	Thr	Ser	His	Gly	Val	His	Trp	Val	Arg	Gln	Ser	Pro	
	65				70					75					80	
gga	aag	ggg	ctg	gag	tgg	ctg	gga	gtg	ata	tgg	ggg	gct	gga	agg	aca	288
Gly	Lys	Gly	Leu	Glu	Trp	Leu	Gly	Val	Ile	Trp	Gly	Ala	Gly	Arg	Thr	
			85					90						95		
gac	tat	aat	gca	gct	ttc	ata	tcc	aga	ctg	agc	atc	agc	agg	gac	att	336
Asp	Tyr	Asn	Ala	Ala	Phe	Ile	Ser	Arg	Leu	Ser	Ile	Ser	Arg	Asp	Ile	
			100					105					110			
tcc	aag	agc	caa	gtt	ttc	ttt	aag	atg	aac	agt	ctg	caa	gtt	gat	gac	384
Ser	Lys	Ser	Gln	Val	Phe	Phe	Lys	Met	Asn	Ser	Leu	Gln	Val	Asp	Asp	
		115					120					125				
aca	gcc	ata	tat	tac	tgt	gcc	aga	aat	agg	tac	gag	agc	tac	ttt	gac	432
Thr	Ala	Ile	Tyr	Tyr	Cys	Ala	Arg	Asn	Arg	Tyr	Glu	Ser	Tyr	Phe	Asp	
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tac	tgg	ggc	caa	ggg	acc	acg	gtc	acc	gtc	tcc	tca	ggg	gga	ggc	ggg	480
Tyr	Trp	Gly	Gln	Gly	Thr	Thr	Val	Thr	Val	Ser	Ser	Gly	Gly	Gly	Gly	
	145				150					155					160	
tca	ggc	gga	ggg	ggc	tct	ggc	ggg	ggc	gga	tgc	gac	atc	gag	ctc	act	528
Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Asp	Ile	Glu	Leu	Thr	
			165				170							175		
cag	tct	cca	ctc	tcc	ctg	cct	gtc	agt	ctt	gga	gat	cag	gcc	tcc	atc	576
Gln	Ser	Pro	Leu	Ser	Leu	Pro	Val	Ser	Leu	Gly	Asp	Gln	Ala	Ser	Ile	
			180					185					190			
tct	tgc	aga	tct	agt	cag	aac	ctt	gta	cac	agt	aat	gga	aat	acc	tat	624
Ser	Cys	Arg	Ser	Ser	Gln	Asn	Leu	Val	His	Ser	Asn	Gly	Asn	Thr	Tyr	
		195				200						205				
tta	cat	tgg	tac	ctg	cag	aag	cca	ggc	cag	tct	cca	aat	ctc	ctg	atc	672
Leu	His	Trp	Tyr	Leu	Gln	Lys	Pro	Gly	Gln	Ser	Pro	Asn	Leu	Leu	Ile	
	210					215					220					
tac	aaa	gtt	tcc	aac	cga	ttt	tct	ggg	gtc	cca	gac	agg	ttc	agt	ggc	720
Tyr	Lys	Val	Ser	Asn	Arg	Phe	Ser	Gly	Val	Pro	Asp	Arg	Phe	Ser	Gly	
	225				230					235					240	

agt Ser	gga Gly	tca Ser	ggg Gly	aca Thr 245	gaa Glu	ttc Phe	aca Thr	ctc Leu	aag Lys 250	atc Ile	agc Ser	aga Arg	gtg Val 255	gag Glu	gct Ala	768
gag Glu	gat Asp	ctg Leu	gga Gly 260	gtt Val	tat Tyr	ttc Phe	tgc Cys	tct Ser 265	caa Gln	agt Ser	aca Thr	cat His	gtt Val 270	ccg Pro	ctc Leu	816
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gcg Ala	ccg Pro 290	gtg Val	ccg Pro	tat Tyr	ccg Pro	gat Asp 295	ccg Pro	ctg Leu	gaa Glu	ccg Pro	cgt Arg 300	gcc Ala	gca Ala	tag		909
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aac Asn	gtg Val	aaa Lys	aaa Lys 20	tta Leu	tta Leu	ttc Phe	gca Ala	att Ile 25	cct Pro	tta Leu	gtt Val	gtt Val	cct Pro 30	ttc Phe	tat Tyr	96
gcg Ala	gcc Ala	cag Gln 35	ccg Pro	gcc Ala	atg Met	gcc Ala	cag Gln 40	gtg Val	aag Lys	ctg Leu	cag Gln	cag Gln 45	tct Ser	gga Gly	cct Pro	144
ggc Gly	cta Leu 50	gtg Val	cag Gln	ccc Pro	tca Ser	cag Gln 55	agc Ser	ctg Leu	tcc Ser	ttc Phe	atc Ile 60	tgc Cys	aca Thr	gtc Val	tct Ser	192
ggc Gly 65	ttc Phe	tca Ser	tta Leu	act Thr	agt Ser 70	cat His	ggc Gly	gta Val	cac His	tgg Trp 75	gtt Val	cgc Arg	cag Gln	tct Ser	cca Pro 80	240
gga Gly	aag Lys	ggc Gly	ctg Leu	gag Glu 85	tgg Trp	ctg Leu	gga Gly	gtg Val	ata Ile 90	tgg Trp	ggc Gly	gct Ala	gga Gly	agg Arg 95	aca Thr	288
gac Asp	tat Tyr	aat Asn	gca Ala 100	gct Ala	ttc Phe	ata Ile	tcc Ser	aga Arg 105	ctg Leu	agc Ser	atc Ile	agc Ser	agg Arg 110	gac Asp	att Ile	336
tcc Ser	aag Lys 115	agc Ser	caa Gln	gtt Val	ttc Phe	ttt Phe	aag Lys 120	atg Met	aac Asn	agt Ser	ctg Leu	caa Gln 125	gtt Val	gat Asp	gac Asp	384

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aca gcc ata tat tac tgt gcc aga aat agg tac gag agc tac ttt gac 432
Thr Ala Ile Tyr Tyr Cys Ala Arg Asn Arg Tyr Glu Ser Tyr Phe Asp
130 135 140

tac tgg ggc caa ggg acc acg gtc acc gtc tcc tca ggt gga ggc ggt 480
Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly
145 150 155 160

tca ggc gga ggt ggc tct ggc ggt ggc gga tcc gac atc gag ctc act 528
Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Glu Leu Thr
165 170 175

cag tct cca ctc tcc ctg cct gtc agt ctt gga gat cag gcc tcc atc 576
Gln Ser Pro Leu Ser Leu Pro Val Ser Leu Gly Asp Gln Ala Ser Ile
180 185 190

tct tgc aga tct agt cag aac ctt gta cac agt aat gga aat acc tat 624
Ser Cys Arg Ser Ser Gln Asn Leu Val His Ser Asn Gly Asn Thr Tyr
195 200 205

tta cat tgg tac ctg cag aag cca ggc cag tct cca aat ctc ctg atc 672
Leu His Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Asn Leu Leu Ile
210 215 220

tac aaa gtt tcc aac cga ttt tct ggg gtc cca gac agg ttc agt ggc 720
Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly
225 230 235 240

agt gga tca ggg aca gaa ttc aca ctc aag atc agc aga gtg gag gct 768
Ser Gly Ser Gly Thr Glu Phe Thr Leu Lys Ile Ser Arg Val Glu Ala
245 250 255

gag gat ctg gga gtt tat ttc tgc tct caa agt aca cat gtt ccg ctc 816
Glu Asp Leu Gly Val Tyr Phe Cys Ser Gln Ser Thr His Val Pro Leu
260 265 270

acg ttc ggt gct ggg acc aag gtg gag ctg aaa cgg gcg gcc gca ggt 864
Thr Phe Gly Ala Gly Thr Lys Val Glu Leu Lys Arg Ala Ala Ala Gly
275 280 285

gcg ccg gtg ccg tat ccg gat ccg ctg gaa ccg cgt gcc gca aag aag 912
Ala Pro Val Pro Tyr Pro Asp Pro Leu Glu Pro Arg Ala Ala Lys Lys
290 295 300

aag tag 918
Lys
305

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&lt;210&gt; 43

&lt;211&gt; 5

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Amino acid  
sequence of heavy chain CDR-1

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<220>
<223> Description of Artificial Sequence: Amino acid
sequence of light chain CDR-2
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&lt;400&gt; 47

Lys Val Ser Asn Arg Phe Ser Gly Val Pro Asp Arg Phe  
 1 5 10

&lt;210&gt; 48

&lt;211&gt; 9

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Amino acid  
 sequence of light chain CDR-3

&lt;400&gt; 48

Ser Gln Ser Thr His Val Pro Leu Thr  
 1 5

&lt;210&gt; 49

&lt;211&gt; 30

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: Primer

&lt;400&gt; 49

gtcccaggat cctctgaagc agtcaggccc

30

&lt;210&gt; 50

&lt;211&gt; 30

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: Primer

&lt;400&gt; 50

acagtggggc cgtcgttttg gctgaggaga

30

&lt;210&gt; 51

&lt;211&gt; 32

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: Primer

&lt;400&gt; 51

tgtgccctcg aggtgactca aactccactc tc

32

&lt;210&gt; 52

&lt;211&gt; 28

&lt;212&gt; DNA

27

<210> 57  
 <211> 32  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Primer

<400> 57  
 tcgagctcac tcagtcctcca ctctccctgc ct

32

<210> 58  
 <211> 25  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Primer

<400> 58  
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25

<210> 59  
 <211> 305  
 <212> PRT  
 <213> Mus sp.

<400> 59  
 Met Lys Tyr Leu Leu Pro Thr Ala Ala Gly Leu Leu Leu Leu Ala  
 1 5 10 15  
 Ala Gln Pro Ala Met Ala Asp Ile Val Leu Thr Gln Ser Pro Ala Ser  
 20 25 30  
 Leu Ala Val Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys Lys Ala Ser  
 35 40 45  
 Gln Ser Val Asp Tyr Asp Gly Asp Ser Tyr Met Asn Trp Tyr Gln Gln  
 50 55 60  
 Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Ala Ala Ser Asn Leu  
 65 70 75 80  
 Glu Ser Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp  
 85 90 95  
 Phe Thr Leu Asn Ile His Pro Val Glu Glu Glu Asp Ala Ala Thr Tyr  
 100 105 110  
 Tyr Cys Gln Gln Ser Ser Glu Asp Pro Pro Thr Phe Gly Gly Gly Thr  
 115 120 125  
 Lys Leu Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly  
 130 135 140

Gly Gly Gly Ser Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val  
145 150 155 160

Lys Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr  
165 170 175

Phe Thr Asp Tyr Val Ile Asn Trp Leu Asn Gln Arg Thr Gly Gln Gly  
180 185 190

Leu Glu Trp Ile Gly Glu Ile Tyr Pro Gly Ser Gly Ser Ala Tyr Tyr  
195 200 205

Asn Glu Met Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser  
210 215 220

Asn Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala  
225 230 235 240

Val Tyr Phe Cys Ala Arg Arg Gly Thr Gly Thr Gly Phe Ala Tyr Trp  
245 250 255

Gly Arg Gly Thr Leu Val Thr Val Ser Ala Ala Ala Ala Asp Tyr Lys  
260 265 270

Asp Asp Asp Asp Lys Gly Ser Ser Glu Gln Lys Leu Ile Ser Glu Glu  
275 280 285

Asp Leu Gly Ser Arg Ser Thr His His His His His His Gly Ser Thr  
290 295 300

Lys  
305

<210> 60

<211> 305

<212> PRT

<213> Mus sp.

<400> 60

Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Ala  
1 5 10 15

Ala Gln Pro Ala Met Ala Gln Val Gln Leu Gln Gln Ser Gly Pro Glu  
20 25 30

Leu Val Lys Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly  
35 40 45

Tyr Thr Phe Thr Asp Tyr Val Ile Asn Trp Leu Asn Gln Arg Thr Gly  
50 55 60

Gln Gly Leu Glu Trp Ile Gly Glu Ile Tyr Pro Gly Ser Gly Ser Ala  
65 70 75 80

Tyr Tyr Asn Glu Met Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys  
85 90 95



Ser Ser Asn Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp  
 100 105 110  
 Ser Ala Val Tyr Phe Cys Ala Arg Arg Gly Thr Gly Thr Gly Phe Ala  
 115 120 125  
 Tyr Trp Gly Arg Gly Thr Leu Val Thr Val Ser Ala Gly Gly Gly Gly  
 130 135 140  
 Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Val Leu Thr  
 145 150 155 160  
 Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly Gln Arg Ala Thr Ile  
 165 170 175  
 Ser Cys Lys Ala Ser Gln Ser Val Asp Tyr Asp Gly Asp Ser Tyr Met  
 180 185 190  
 Asn Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr  
 195 200 205  
 Ala Ala Ser Asn Leu Glu Ser Gly Ile Pro Ala Arg Phe Ser Gly Ser  
 210 215 220  
 Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His Pro Val Glu Glu Glu  
 225 230 235 240  
 Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Ser Ser Glu Asp Pro Pro Thr  
 245 250 255  
 Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Ala Ala Ala Asp Tyr Lys  
 260 265 270  
 Asp Asp Asp Asp Lys Gly Ser Ser Glu Gln Lys Leu Ile Ser Glu Glu  
 275 280 285  
 Asp Leu Gly Ser Arg Ser Thr His His His His His Gly Ser Thr  
 290 295 300

Lys  
 305

<210> 61  
 <211> 118  
 <212> PRT  
 <213> Mus sp.

<400> 61

Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala  
 1 5 10 15  
 Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr  
 20 25 30  
 Val Ile Asn Trp Leu Asn Gln Arg Thr Gly Gln Gly Leu Glu Trp Ile  
 35 40 45

Gly Glu Ile Tyr Pro Gly Ser Gly Ser Ala Tyr Tyr Asn Glu Met Phe  
 50 55 60  
 Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Asn Thr Ala Tyr  
 65 70 75 80  
 Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys  
 85 90 95  
 Ala Arg Arg Gly Thr Gly Thr Gly Phe Ala Tyr Trp Gly Arg Gly Thr  
 100 105 110  
 Leu Val Thr Val Ser Ala  
 115

<210> 62  
 <211> 111  
 <212> PRT  
 <213> Mus sp.

<400> 62  
 Asp Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly  
 1 5 10 15  
 Gln Arg Ala Thr Ile Ser Cys Lys Ala Ser Gln Ser Val Asp Tyr Asp  
 20 25 30  
 Gly Asp Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro  
 35 40 45  
 Lys Leu Leu Ile Tyr Ala Ala Ser Asn Leu Glu Ser Gly Ile Pro Ala  
 50 55 60  
 Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His  
 65 70 75 80  
 Pro Val Glu Glu Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Ser Ser  
 85 90 95  
 Glu Asp Pro Pro Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys  
 100 105 110

<210> 63  
 <211> 117  
 <212> PRT  
 <213> Mus sp.

<400> 63  
 Gln Val Gln Leu Lys Gln Ser Gly Pro Gly Leu Val Gln Pro Ser Gln  
 1 5 10 15  
 Ser Leu Ser Phe Ile Cys Thr Val Ser Gly Phe Ser Leu Thr Ser His  
 20 25 30  
 Gly Val His Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Leu  
 35 40 45

Gly Val Ile Trp Gly Ala Gly Arg Thr Asp Tyr Asn Ala Ala Phe Ile  
50 55 60

Ser Arg Leu Ser Ile Ser Arg Asp Ile Ser Lys Ser Gln Val Phe Phe  
65 70 75 80

Lys Met Asn Ser Leu Gln Val Asp Asp Thr Ala Ile Tyr Tyr Cys Ala  
85 90 95

Arg Asn Arg Tyr Glu Ser Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Thr  
100 105 110

Ser Leu Thr Val Ser  
115

<210> 64

<211> 113

<212> PRT

<213> Mus sp.

<400> 64

Asp Val Val Met Thr Gln Thr Pro Leu Ser Leu Pro Val Ser Leu Gly  
1 5 10 15

Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Asn Leu Val His Ser  
20 25 30

Asn Gly Asn Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro Gly Gln Ser  
35 40 45

Pro Asn Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro  
50 55 60

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Lys Ile  
65 70 75 80

Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Phe Cys Ser Gln Ser  
85 90 95

Thr His Val Pro Leu Thr Phe Gly Ala Gly Thr Lys Val Glu Leu Lys  
100 105 110

Arg

<210> 65

<211> 302

<212> PRT

<213> Mus sp.

<400> 65

Met Thr Met Ile Thr Pro Ser Phe Gly Ala Phe Phe Leu Glu Ile Phe  
1 5 10 15

Asn Val Lys Lys Leu Leu Phe Ala Ile Pro Leu Val Val Pro Phe Tyr  
20 25 30

Ala Ala Gln Pro Ala Met Ala Gln Val Lys Leu Gln Gln Ser Gly Pro  
           35                          40                          45  
 Gly Leu Val Gln Pro Ser Gln Ser Leu Ser Phe Ile Cys Thr Val Ser  
           50                          55                          60  
 Gly Phe Ser Leu Thr Ser His Gly Val His Trp Val Arg Gln Ser Pro  
           65                          70                          75                          80  
 Gly Lys Gly Leu Glu Trp Leu Gly Val Ile Trp Gly Ala Gly Arg Thr  
                           85                          90                          95  
 Asp Tyr Asn Ala Ala Phe Ile Ser Arg Leu Ser Ile Ser Arg Asp Ile  
                           100                          105                          110  
 Ser Lys Ser Gln Val Phe Phe Lys Met Asn Ser Leu Gln Val Asp Asp  
           115                          120                          125  
 Thr Ala Ile Tyr Tyr Cys Ala Arg Asn Arg Tyr Glu Ser Tyr Phe Asp  
           130                          135                          140  
 Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly  
           145                          150                          155                          160  
 Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Glu Leu Thr  
                           165                          170                          175  
 Gln Ser Pro Leu Ser Leu Pro Val Ser Leu Gly Asp Gln Ala Ser Ile  
                           180                          185                          190  
 Ser Cys Arg Ser Ser Gln Asn Leu Val His Ser Asn Gly Asn Thr Tyr  
           195                          200                          205  
 Leu His Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Asn Leu Leu Ile  
           210                          215                          220  
 Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly  
           225                          230                          235                          240  
 Ser Gly Ser Gly Thr Glu Phe Thr Leu Lys Ile Ser Arg Val Glu Ala  
                           245                          250                          255  
 Glu Asp Leu Gly Val Tyr Phe Cys Ser Gln Ser Thr His Val Pro Leu  
           260                          265                          270  
 Thr Phe Gly Ala Gly Thr Lys Val Glu Leu Lys Arg Ala Ala Ala Gly  
           275                          280                          285  
 Ala Pro Val Pro Tyr Pro Asp Pro Leu Glu Pro Arg Ala Ala  
           290                          295                          300

<210> 66  
 <211> 305  
 <212> PRT  
 <213> Mus sp.

Met 1	Thr	Met	Ile	Thr 5	Pro	Ser	Phe	Gly	Ala 10	Phe	Phe	Leu	Glu	Ile 15	Phe
Asn	Val	Lys	Lys 20	Leu	Leu	Phe	Ala	Ile 25	Pro	Leu	Val	Val	Pro 30	Phe	Tyr
Ala	Ala	Gln 35	Pro	Ala	Met	Ala	Gln 40	Val	Lys	Leu	Gln	Gln	Ser 45	Gly	Pro
Gly	Leu 50	Val	Gln	Pro	Ser	Gln 55	Ser	Leu	Ser	Phe	Ile 60	Cys	Thr	Val	Ser
Gly 65	Phe	Ser	Leu	Thr	Ser 70	His	Gly	Val	His	Trp 75	Val	Arg	Gln	Ser	Pro 80
Gly	Lys	Gly	Leu	Glu 85	Trp	Leu	Gly	Val	Ile 90	Trp	Gly	Ala	Gly	Arg 95	Thr
Asp	Tyr	Asn 100	Ala	Ala	Phe	Ile	Ser	Arg 105	Leu	Ser	Ile	Ser	Arg 110	Asp	Ile
Ser	Lys	Ser 115	Gln	Val	Phe	Phe	Lys 120	Met	Asn	Ser	Leu	Gln	Val	Asp	Asp
Thr 130	Ala	Ile	Tyr	Tyr	Cys 135	Ala	Arg	Asn	Arg	Tyr	Glu 140	Ser	Tyr	Phe	Asp
Tyr 145	Trp	Gly	Gln	Gly	Thr 150	Thr	Val	Thr	Val	Ser 155	Ser	Gly	Gly	Gly	Gly 160
Ser	Gly	Gly	Gly 165	Gly	Ser	Gly	Gly	Gly	Gly 170	Ser	Asp	Ile	Glu	Leu 175	Thr
Gln	Ser	Pro 180	Leu	Ser	Leu	Pro	Val	Ser 185	Leu	Gly	Asp	Gln	Ala 190	Ser	Ile
Ser	Cys 195	Arg	Ser	Ser	Gln	Asn	Leu 200	Val	His	Ser	Asn	Gly 205	Asn	Thr	Tyr
Leu 210	His	Trp	Tyr	Leu	Gln	Lys 215	Pro	Gly	Gln	Ser	Pro 220	Asn	Leu	Leu	Ile
Tyr 225	Lys	Val	Ser	Asn 230	Arg	Phe	Ser	Gly	Val	Pro 235	Asp	Arg	Phe	Ser	Gly 240
Ser	Gly	Ser	Gly 245	Thr	Glu	Phe	Thr	Leu	Lys 250	Ile	Ser	Arg	Val	Glu 255	Ala
Glu	Asp	Leu 260	Gly	Val	Tyr	Phe	Cys	Ser 265	Gln	Ser	Thr	His	Val 270	Pro	Leu
Thr	Phe 275	Gly	Ala	Gly	Thr	Lys	Val 280	Glu	Leu	Lys	Arg	Ala 285	Ala	Ala	Gly
Ala	Pro 290	Val	Pro	Tyr	Pro	Asp 295	Pro	Leu	Glu	Pro	Arg 300	Ala	Ala	Lys	Lys

Lys  
305

[illegible]